09/578,507
AU 13

WEST Search History

DATE: Thursday, March 13, 2003

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ		
L3	l1 with L2	325	L3
L2	dna or rna or plasmid or oligonucleotide or polynucleotide or (nucleic acid)	195270	L2
L1	hydrophobic interaction	7813	L1

END OF SEARCH HISTORY

WEST

Print Selection

Help | Clear | Cancel | Print | Print First Page

Select?	Document ID	Section(s)	Page(s)	# Pages to print	Database
☑	20010007026	all	all	15	USPT,PGPB,JPAB,EPAB,DWPI
☑	EP000964057A1	all	all	N/A	USPT,PGPB,JPAB,EPAB,DWPI
☑	5610287	all	all	25	USPT,PGPB,JPAB,EPAB,DWPI
☑	4427580	all	all	5	USPT,PGPB,JPAB,EPAB,DWPI
☑	EP792281B	all	all	N/A	USPT,PGPB,JPAB,EPAB,DWPI
☑	EP964057A	all	all	N/A	USPT,PGPB,JPAB,EPAB,DWPI
☑	WO9601268A	all	all	N/A	USPT,PGPB,JPAB,EPAB,DWPI

Building	Room	Printer
cm1	11e14	gbldptr

Main Menu | Logout

09/578,507
Att B

=> s hydrophobic interaction
L1 15076 HYDROPHOBIC INTERACTION

=> s plasmid?
L2 349443 PLASMID?

=> s l1 and l2

L3 278 L1 AND L2

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 154 DUP REM L3 (124 DUPLICATES REMOVED)

=> s l4 and py<2000

1 FILES SEARCHED...
3 FILES SEARCHED...
4 FILES SEARCHED...
L5 106 L4 AND PY<2000

=> d l5 ibib abs 1-106

L5 ANSWER 1 OF 106 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:134598 BIOSIS
DOCUMENT NUMBER: PREV200000134598
TITLE: Separation and analysis of ***plasmid*** denatured forms using ***hydrophobic*** ***interaction*** chromatography.
AUTHOR(S): Diogo, M. M.; Queiroz, J. A.; Monteiro, G. A.; Prazeres, D.M.F. (1)
CORPORATE SOURCE: (1) Centro de Engenharia Biologica e Quimica, Instituto
Superior Tecnico, 1000, Lisbon Portugal
SOURCE: Analytical Biochemistry., (***Nov. 1, 1999***) Vol. 275, No. 1, pp. 122-124.
ISSN: 0003-2697.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L5 ANSWER 2 OF 106 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:536474 BIOSIS
DOCUMENT NUMBER: PREV199900536474
TITLE: Expression and partial purification of a recombinant secretory form of human liver carboxylesterase.
AUTHOR(S): Miller, Amanda D. (1); Scott, David F.; Chacko, Terry L.;
Maxwell, Donald M.; Schlager, John J.; Lanclos, Kenneth D. (1)
CORPORATE SOURCE: (1) Department of Biochemistry and Molecular Biology,
Medical College of Georgia, Augusta, GA, 30912 USA
SOURCE: Protein Expression and Purification, (***Oct., 1999***) Vol. 17, No. 1, pp. 16-25.
ISSN: 1046-5928.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Serine-dependent carboxylesterases (EC 3.1.1.1) are found in a variety of
tissues with high activity detected in the liver. Carboxylesterases (CaE) hydrolyze aliphatic and aromatic esters, and aromatic amides, and play an important role in the detoxification of xenobiotic chemicals that contain organophosphate (OP) compounds. The detoxifying ability of CaE is limited
by its low concentration in serum where it encounters OP compounds. Studies in our laboratory have shown that a pRC/CMV-hCaE ***plasmid***
construct, stably integrated into 293T cells, expresses a human liver CaE in culture. However, the enzyme remained inside the cell and reached a low
steady-state level of expression. The goals of this study were to overexpress a functional human liver CaE from a recombinant cDNA in a human cell line and to isolate and purify the recombinant protein. To accomplish these goals, a single amino acid change was made in the C-terminal retrieval signal, HIEL (His-Ile-Glu-Leu), of human liver CaE. The mutation produced a unique Eco47III restriction site, which aided in clone selection. The recombinant ***plasmid*** , pRc/CMV-mhCaE, was
isolated and stably integrated into human 293T cells. Expression of the altered cDNA resulted in secretion of an active CaE up to levels of 500 enzyme units per liter of growth medium. Secretory CaE displayed isoelectric focusing patterns similar to those of the native enzyme with no observable changes in activity. The secreted enzyme was partially purified by ***hydrophobic*** ***interaction*** chromatography and
Cibacron blue affinity chromatography. Partial enzyme purification was achieved, and CaE retained a high level of enzymatic activity.

L5 ANSWER 3 OF 106 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:226641 BIOSIS
DOCUMENT NUMBER: PREV199900226641
TITLE: The CREB constitutive activation domain interacts with TATA-binding protein-associated factor 110 (TAF110) through specific hydrophobic residues in one of the three subdomains required for both activation and TAF110 binding.
AUTHOR(S): Felinski, Edward A.; Quinn, Patrick G. (1)
CORPORATE SOURCE: (1) Dept. of Cellular and Molecular Physiology, H166, The
Pennsylvania State University College of Medicine, 500 University Dr., Hershey, PA, 17033 USA
SOURCE: Journal of Biological Chemistry, (***April 23, 1999***) Vol. 274, No. 17, pp. 11672-11678.
ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The cAMP response element-binding protein (CREB) mediates both basal and
PKA-inducible transcription through two separate and independently active
domains, the constitutive activation domain (CAD) and the kinase-inducible
domain, respectively. The CREB CAD interacts with the general transcription factor TFIID through one or more of the TATA-binding protein-associated factors (TAFs), one of which is TAF110. The CAD is composed of three subdomains, rich in either serine, hydrophobic amino acids, or glutamine. In the present study, analysis of deletion mutants of the CAD showed that all three CAD subdomains were required for effective
interaction with TAF110 in a yeast two-hybrid assay. Therefore, a library of random point mutations within the CAD was analyzed in a reverse two-hybrid screen to identify amino acids that are essential for interaction with the TAF. Interaction defects resulted solely from mutations of hydrophobic amino acid residues within the hydrophobic cluster to charged amino acid residues. Together, the deletion and mutation analyses suggest that the entire CAD provides an environment for
a specific ***hydrophobic*** ***interaction*** with TAF110 that is crucial for interaction. Our results provide further evidence for a model of basal activation by CREB involving interaction with TAF110 that promotes recruitment or stabilization of TFIID binding to the promoter, which facilitates pre-initiation complex assembly.

L5 ANSWER 4 OF 106 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:203502 BIOSIS
DOCUMENT NUMBER: PREV199900203502
TITLE: Purification and characterization of a mitochondrial thymine glycol endonuclease from rat liver.
AUTHOR(S): Stierum, Rob H.; Croteau, Deborah L.; Bohr, Vilhelm A. (1)
CORPORATE SOURCE: (1) Laboratory of Molecular Genetics, NIA, National
Institutes of Health, 5600 Nathan Shock Dr., Baltimore, MD, 21224 USA
SOURCE: Journal of Biological Chemistry, (***March 12, 1999***)
Vol. 274, No. 11, pp. 7128-7136.
ISSN: 0021-9258.
DOCUMENT TYPE: Article